Claims

1. A reagent for predicting a phospholipidosis induction potential of a compound, which comprises a nucleic acid capable of hybridizing to a nucleic acid having a base sequence shown by any of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21 and 23 under high stringent conditions and/or a nucleic acid capable of hybridizing to a nucleic acid having a base sequence complementary to the base sequence under high stringent conditions.

2. A kit for predicting a phospholipidosis induction potential of a compound, which comprises one or more reagents containing a nucleic acid capable of hybridizing to a transcription product of a gene showing varying expression in correlation with expression of phospholipidosis under high stringent conditions and/or a nucleic acid capable of hybridizing to a nucleic acid having a base sequence complementary to the transcription product under high stringent conditions, wherein, when two or more reagents are contained, each reagent can detect expression of different genes.

3. The kit of claim 2, wherein at least one reagent comprises a nucleic acid capable of hybridizing to a nucleic acid having a base sequence shown by any of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21 and 23 under high stringent conditions and/or a nucleic acid capable of hybridizing to a nucleic acid having a base sequence complementary to the base sequence under high stringent conditions.

4. The kit of claim 2, wherein a prediction hitting ratio of the phospholipidosis induction potential is not less than about 70% when a mammalian cell is exposed to a test compound, using an average variation rate of expression of a nucleic acid, to which the nucleic acid contained in each reagent is capable of

hybridizing, in said cell as an index.

5. A method for predicting a phospholipidosis induction potential of a compound, which comprises detecting expression variation of one or more genes showing expression variation in correlation with phospholipidosis expression, in a sample containing a mammalian cell exposed to the compound or a sample taken from a mammal administered with the compound.

6. The method of claim 5, wherein at least one gene has the same or substantially the same base sequence as the base sequence shown by any of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21 and 23.

7. A method for determining the standard for the judgment of the presence or absence of a phospholipidosis induction potential of a compound, which comprises
(1) detecting expression variation of one or more genes showing expression variation in correlation with phospholipidosis expression, in samples containing a mammalian cell exposed to each of two or more known phospholipidosis-inducing compounds and two or more known phospholipidosis non-inducing compounds or samples taken from mammals administered with each of said compounds, and
(2) using, as a standard value, an average variation rate capable of correctly judging the presence or absence of a phospholipidosis induction potential of the above-mentioned compounds by not less than about 70% based on the relationship between an average expression variation rate of the genes and the phospholipidosis induction potential.

8. The method of claim 7, wherein at least one gene has the same or substantially the same base sequence as the base sequence shown by any of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21 and 23.

9. The method of claim 7, further comprising examining validity of the standard value using other known phospholipidosis inducing compound and known phospholipidosis non-inducing compound.

10. The method of claim 5, comprising comparing the average variation rate of gene expression with the standard value obtained by the method of claim 7 or 9.

11. A method for predicting the toxicity of a compound, which comprises,

(1) detecting expression variation of one or more genes showing expression variation in correlation with toxicity expression, in a sample containing a mammalian cell exposed to the compound or a sample taken from a mammal administered with the compound, and

(2) judging the presence or absence of toxicity of the compound with an average variation rate of the gene expression as an index.